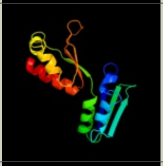
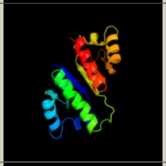
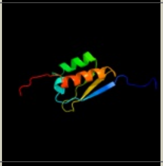
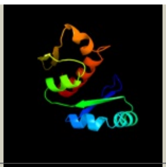
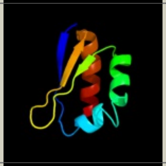
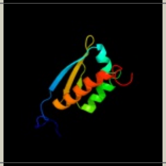
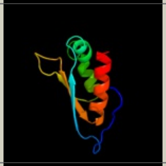
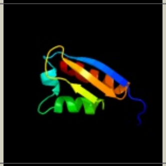
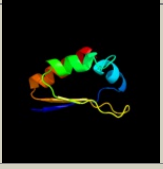
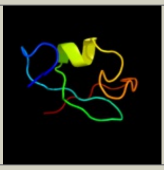
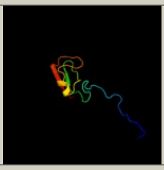
Phyre^2

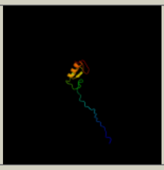
Email	l.a.kelley@imperial.ac.uk
Description	A1L020
Date	Tue Apr 3 15:04:20 BST 2012
Unique Job ID	1d9613f1f7c6b66e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n89B_	Alignment		100.0	18	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**defective in germ line development protein 3, isoform a; **PDBTitle:** kh domains
2	c1tuaA_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ape0754; **PDBTitle:** 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix
3	c2jvzA_	Alignment		99.9	23	**PDB header:**splicing **Chain:** A: **PDB Molecule:**far upstream element-binding protein 2; **PDBTitle:** solution nmr structure of the second and third kh domains2 of ksrp
4	c2qndA_	Alignment		99.9	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**fmr1 protein; **PDBTitle:** crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein
5	c2e3uA_	Alignment		99.9	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein ph1566; **PDBTitle:** crystal structure analysis of dim2p from pyrococcus horikoshii ot3
6	c2jzxA_	Alignment		99.9	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
7	c3krmB_	Alignment		99.9	24	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**insulin-like growth factor 2 mrna-binding protein **PDBTitle:** imp1 kh34
8	c1j4wA_	Alignment		99.9	28	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**fuse binding protein; **PDBTitle:** complex of the kh3 and kh4 domains of fbp with a2 single_stranded 29mer dna oligonucleotide from the fuse3 element of the c-myc oncogene
9	c2anrA_	Alignment		99.9	25	**PDB header:**rna-binding protein/rna **Chain:** A: **PDB Molecule:**neuro-oncological ventral antigen 1; **PDBTitle:** crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin
10	c2dgrA_	Alignment		99.7	67	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ring finger and kh domain-containing protein 1; **PDBTitle:** solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
11	d2ctma1	Alignment		99.5	25	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)

12	c2cy1A_	Alignment		99.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nusa protein homolog; **PDBTitle:** crystal structure of ape1850
13	d2ctka1	Alignment		99.5	28	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
14	d2ctea1	Alignment		99.5	23	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
15	d1viga_	Alignment		99.5	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
16	d1khma_	Alignment		99.4	20	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
17	d1we8a_	Alignment		99.4	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
18	d1wvna1	Alignment		99.4	25	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
19	d1x4na1	Alignment		99.4	26	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
20	d2axya1	Alignment		99.4	20	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
21	d1x4ma1	Alignment	not modelled	99.4	30	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
22	c3t6pA_	Alignment		99.4	38	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 2; **PDBTitle:** iap antagonist-induced conformational change in ciap1 promotes e32 ligase activation via dimerization
23	d2ctfa1	Alignment	not modelled	99.4	23	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
24	d2ctja1	Alignment	not modelled	99.4	19	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
25	c1ztgD_	Alignment	not modelled	99.4	23	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
26	d2ctla1	Alignment	not modelled	99.4	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
27	d1j4wa1	Alignment	not modelled	99.4	32	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
28	d1ec6a_	Alignment	not modelled	99.4	24	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I)

						Family: Eukaryotic type KH-domain (KH-domain type I)
29	d1zzka1	Alignment	not modelled	99.4	24	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
30	d1dtja_	Alignment	not modelled	99.4	26	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
31	c2hh2A_	Alignment	not modelled	99.3	29	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the fourth kh domain of ksrp
32	d1j4wa2	Alignment	not modelled	99.3	34	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
33	c2hh3A_	Alignment	not modelled	99.3	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the third kh domain of ksrp
34	d1dt4a_	Alignment	not modelled	99.3	27	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
35	d2ba0a3	Alignment	not modelled	99.2	24	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
36	d1tuaa1	Alignment	not modelled	99.1	25	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
37	c2ecgA_	Alignment		99.0	34	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** solution structure of the ring domain of the baculoviral2 iap repeat-containing protein 4 from homo sapiens
38	d1tuaa2	Alignment	not modelled	98.9	26	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
39	c2ea5A_	Alignment		98.9	27	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell growth regulator with ring finger domain **PDBTitle:** solution structure of the ring domain of the human cell2 growth regulator with ring finger domain 1 protein
40	c2yhoE_	Alignment	not modelled	98.9	35	**PDB header:**ligase **Chain:** E: **PDB Molecule:**e3 ubiquitin-protein ligase mylip; **PDBTitle:** the idol-ube2d complex mediates sterol-dependent degradation of the2 ldl receptor
41	c2vjfB_	Alignment	not modelled	98.9	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**mdm4 protein; **PDBTitle:** crystal structure of the mdm2-mdmx ring domain heterodimer
42	c3eb6A_	Alignment	not modelled	98.9	38	**PDB header:**apoptosis, ligase **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 3; **PDBTitle:** structure of the ciap2 ring domain bound to ubch5b
43	c2d8tA_	Alignment	not modelled	98.9	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 146; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 146
44	c2yqrA_	Alignment	not modelled	98.8	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0907 protein; **PDBTitle:** solution structure of the kh domain in kiaa0907 protein
45	c3fl2A_	Alignment	not modelled	98.8	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
46	c1z6uA_	Alignment	not modelled	98.8	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**np95-like ring finger protein isoform b; **PDBTitle:** np95-like ring finger protein isoform b [homo sapiens]
47	d2z0sa2	Alignment	not modelled	98.8	22	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
48	c2hdpB_	Alignment	not modelled	98.8	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ubiquitin-protein ligase e3 mdm2; **PDBTitle:** solution structure of hdm2 ring finger domain
49	c2csyA_	Alignment	not modelled	98.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**zinc finger protein 183-like 1; **PDBTitle:** solution structure of the ring domain of the zinc finger2 protein 183-like 1
50	c2ecnA_	Alignment	not modelled	98.7	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 141; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 141
51	c3u1kB_	Alignment	not modelled	98.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyribonucleotide nucleotidyltransferase 1, mitochondrial; **PDBTitle:** crystal structure of human pnpase
52	c2ecyA_	Alignment	not modelled	98.6	21	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
53	c2yslA	Alignment	not modelled	98.6	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 31;

						PDBTitle: solution structure of the ring domain (1-66) from2 tripartite motif-containing protein 31
54	c3l11A_	Alignment	not modelled	98.6	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rnf168; **PDBTitle:** crystal structure of the ring domain of rnf168
55	d1fbva4	Alignment	not modelled	98.6	27	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
56	c2eciA_	Alignment		98.5	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of the human tnf2 receptor-associated factor 6 protein
57	c2ectA_	Alignment	not modelled	98.5	34	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 126; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain of ring finger protein 126
58	c2h0dB_	Alignment	not modelled	98.5	20	**PDB header:**metal binding protein/ligase **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex
59	c1x4jA_	Alignment	not modelled	98.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ring finger protein 38; **PDBTitle:** solution structure of ring finger in ring finger protein 38
60	c2djbA_	Alignment	not modelled	98.5	30	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 6; **PDBTitle:** solution structure of the ring domain of the human polycomb2 group ring finger protein 6
61	c2ea6A_	Alignment	not modelled	98.5	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein 4; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 4
62	c2cklB_	Alignment	not modelled	98.5	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
63	c2jmdA_	Alignment	not modelled	98.5	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of human traf6
64	d1k1ga_	Alignment	not modelled	98.4	33	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
65	d1rmda2	Alignment	not modelled	98.4	28	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
66	d1jm7a_	Alignment	not modelled	98.4	26	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
67	d1chca_	Alignment	not modelled	98.4	33	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
68	d1v87a_	Alignment	not modelled	98.4	27	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
69	c3lrqB_	Alignment	not modelled	98.4	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase trim37; **PDBTitle:** crystal structure of the u-box domain of human ubiquitin-2 protein ligase (e3), northeast structural genomics3 consortium target hr4604d.
70	c2ep4A_	Alignment	not modelled	98.4	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ring finger protein 24; **PDBTitle:** solution structure of ring finger from human ring finger2 protein 24
71	c2ecwA_	Alignment	not modelled	98.4	25	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 30; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain tripartite motif protein 30
72	c2ecjA_	Alignment	not modelled	98.4	35	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 39; **PDBTitle:** solution structure of the ring domain of the human2 tripartite motif-containing protein 39
73	c2ecvA_	Alignment	not modelled	98.3	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 5; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain of tripartite motif-containing protein 5
74	c2kizA_	Alignment	not modelled	98.3	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase arkadia; **PDBTitle:** solution structure of arkadia ring-h2 finger domain
75	c2cklA_	Alignment	not modelled	98.3	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 4; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
76	c2yurA_	Alignment	not modelled	98.3	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6; **PDBTitle:** solution structure of the ring finger of human2 retinoblastoma-binding protein 6
77	c2l0bA_	Alignment	not modelled	98.3	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase praja-1; **PDBTitle:** solution nmr structure of zinc finger domain of e3 ubiquitin-protein2 ligase praja-1 from homo sapiens, northeast structural genomics3 consortium (nesg) target hr4710b
78	d1g25a_	Alignment	not modelled	98.3	23	**Fold:**RING/U-box **Superfamily:**RING/U-box

						Family:RING finger domain, C3HC4
79	d1e4ua_	Alignment	not modelled	98.2	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
80	c2f42A_	Alignment	not modelled	98.2	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
81	c2egpA_	Alignment	not modelled	98.2	25	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 34; **PDBTitle:** solution structure of the ring-finger domain from human2 tripartite motif protein 34
82	c2xeuA_	Alignment	not modelled	98.2	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein 4; **PDBTitle:** ring domain
83	c2ct2A_	Alignment	not modelled	98.2	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tripartite motif protein 32; **PDBTitle:** solution structure of the ring domain of the tripartite2 motif protein 32
84	c3ztgA_	Alignment	not modelled	98.2	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rbbp6; **PDBTitle:** solution structure of the ring finger-like domain of2 retinoblastoma binding protein-6 (rbbp6)
85	c1fbvA_	Alignment	not modelled	98.1	35	**PDB header:**ligase **Chain:** A: **PDB Molecule:**signal transduction protein cbl; **PDBTitle:** structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases
86	d2bl5a1	Alignment	not modelled	98.1	36	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
87	d3dplr1	Alignment	not modelled	98.1	33	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
88	d2fmra_	Alignment	not modelled	98.1	25	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
89	d1bora_	Alignment	not modelled	98.0	30	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
90	c2ct0A_	Alignment	not modelled	98.0	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-smc element 1 homolog; **PDBTitle:** solution structure of the ring domain of the non-smc2 element 1 protein
91	c3vk6A_	Alignment	not modelled	98.0	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hakai; **PDBTitle:** crystal structure of a phosphotyrosine binding domain
92	c2eclA_	Alignment	not modelled	98.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring-box protein 2; **PDBTitle:** solution structure of the ring domain of the human ring-box2 protein 2
93	c3htkC_	Alignment	not modelled	98.0	13	**PDB header:**recombination/replication/ligase **Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21; **PDBTitle:** crystal structure of mms21 and smc5 complex
94	d1t1ha_	Alignment	not modelled	97.9	15	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
95	c2y43B_	Alignment	not modelled	97.9	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18; **PDBTitle:** rad18 ubiquitin ligase ring domain structure
96	d1ur6b_	Alignment	not modelled	97.9	30	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
97	c2ecmA_	Alignment	not modelled	97.9	33	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution structure of the ring domain of the ring finger2 and chy zinc finger domain-containing protein 1 from mus3 musculus
98	d2c2la2	Alignment	not modelled	97.9	17	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
99	c2kreA_	Alignment	not modelled	97.9	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin conjugation factor e4 b; **PDBTitle:** solution structure of e4b/ufd2a u-box domain
100	c3nw0A_	Alignment	not modelled	97.9	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural maintenance of chromosomes element 1 **PDBTitle:** crystal structure of mageg1 and nse1 complex
101	d1jm7b_	Alignment	not modelled	97.9	29	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
102	c2jrjA_	Alignment	not modelled	97.9	34	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain **PDBTitle:** solution structure of the human pirh2 ring-h2 domain.2 northeast structural genomics consortium target ht2b
103	d1iyma_	Alignment	not modelled	97.8	37	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
104	d2baya1	Alignment	not modelled	97.8	11	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box

105	c3knvA_	Alignment	not modelled	97.8	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of the ring and first zinc finger domains2 of traf2
106	c1rmdA_	Alignment	not modelled	97.8	28	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**rag1; **PDBTitle:** rag1 dimerization domain
107	d2c2vv1	Alignment	not modelled	97.8	16	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
108	c3hctA_	Alignment	not modelled	97.7	25	**PDB header:**signaling protein/ligase **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** crystal structure of traf6 in complex with ubc13 in the p12 space group
109	d1wgma_	Alignment	not modelled	97.7	9	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
110	c3hcsA_	Alignment	not modelled	97.6	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** crystal structure of the n-terminal domain of traf6
111	d2cpqa1	Alignment	not modelled	97.4	19	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
112	c2yu4A_	Alignment	not modelled	97.2	22	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**e3 sumo-protein ligase nse2; **PDBTitle:** solution structure of the sp-ring domain in non-smc element2 2 homolog (mms21, s. cerevisiae)
113	c2asbA_	Alignment	not modelled	97.2	15	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
114	c1k0rB_	Alignment	not modelled	97.2	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
115	d1wima_	Alignment	not modelled	97.1	24	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
116	c1l2fA_	Alignment	not modelled	97.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
117	c1hh2P_	Alignment	not modelled	96.9	20	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
118	c2d8sA_	Alignment	not modelled	96.6	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cellular modulator of immune recognition; **PDBTitle:** solution structure of the ring domain of the human cellular2 modulator of immune recognition protein
119	d1vyxa_	Alignment	not modelled	96.1	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Variant RING domain
120	c3gkuB_	Alignment	not modelled	95.9	13	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**probable rna-binding protein; **PDBTitle:** crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940